AMENDMENT

Please amend the subject application as follows:

IN THE CLAIMS:

1. (Currently amended) A method for obtaining *in vivo* binding partners of a protein of interest in a cell type, the method comprising:
   (a) obtaining a cell of said cell type transformed to express a fusion protein, said fusion protein comprising:
      (i) said protein of interest; and
      (ii) a single post-translational modification sequence;
   (b) growing said cell or progeny of said cell under conditions which permit expression and post-translation modification of said fusion protein to produce a singly tagged fusion protein, and allow for contacting of binding partners if present to said protein of interest;
   (c) contacting an extract of said cell or progeny of said cell with an affinity purification reagent which specifically binds to said tagged fusion protein to form a complex;
   (d) separating said complex from said extract; and
   (e) identifying any binding partners that bind said protein of interest in said complex.

2. (Original) The method of claim 1, wherein an enzyme that performs the post-translation modification of said fusion protein is not naturally expressed in the cell of said cell type, and is encoded by a vector which is introduced into the cell.

3. (Original) The method of claim 1, wherein the cell is a mammalian cell.

4. (Canceled)

5. (Previously presented) The method of claim 1, wherein said fusion protein comprises an affinity purification sequence selected from the group consisting of

polyhistidine, *S. aureus* protein A IgG binding domain, glutathione-S-transferase binding domain, maltose binding protein, cellulose binding domain, calmodulin binding peptide, an epitope tag, and combinations thereof.

6. (Previously presented) The method of claim 1, wherein said fusion protein comprises a cleavage site between said protein of interest and said post-translational modification sequence, and said method further comprises the steps of:

(a) cleaving said cleavage site after separating said complex from said extract to form a cleaved protein of interest; and

(b) separating said cleaved protein of interest from said post-translational modification sequence prior to identifying any binding partners of said protein of interest.

7. (Previously presented) The method of claim 1, wherein the protein of interest comprises an affinity purification sequence selected from the group consisting of polyhistidine, *S. aureus* protein A IgG binding domain, glutathione-S-transferase binding domain, maltose binding protein, cellulose binding domain, calmodulin binding peptide, an epitope tag, and combinations thereof, and wherein the affinity purification sequence remains attached to the protein of interest after cleaving said cleavage site.

8. (Previously presented) The method of claim 7, comprising affinity purifying the protein of interest after the separating step.

9. (Currently amended) A method for obtaining *in vivo* binding partners of a protein of interest in a cell type comprising:

(a) transforming a cell of said cell type with a vector encoding a fusion protein, the fusion protein comprising:

(i) said protein of interest;

(ii) a single post-translational modification sequence;

(b) growing said cell or progeny of said cell under conditions which permit expression and post-translation modification of said fusion protein to produce a singly tagged fusion protein, and allow for contacting of binding partners if present to said protein of interest;

(c) contacting an extract of said cell or progeny of said cell with an affinity purification reagent which specifically binds to said tagged fusion protein to form a complex;

(d) separating said complex from said extract; and

(e) identifying any binding partners that bind said protein of interest in said complex.

10. (Original) The method of claim 9, wherein the cell is a mammalian cell.

11. (Canceled)

12. (Original) The method of claim 9, wherein said fusion protein further comprises an affinity purification sequence selected from the group consisting of polyhistidine, *S. aureus* protein A IgG binding domain, glutathione-S-transferase binding domain, maltose binding protein, cellulose binding domain, calmodulin binding peptide, an epitope tag, and combinations thereof.

13. (Previously presented) The method of claim 9, wherein said fusion protein comprises a cleavage site between said protein of interest and said post-translational modification sequence, and said method further comprises the steps of:

(a) cleaving said cleavage site after separating said complex from said extract to form a cleaved protein of interest; and

(b) separating said cleaved protein of interest from said post-translational modification sequence prior to identifying any binding partners of said protein of interest.

14. (Previously presented) The method of claim 9, wherein the protein of interest comprises an affinity purification sequence selected from the group consisting of polyhistidine, *S. aureus* protein A IgG binding domain, glutathione-S-transferase binding domain, maltose binding protein, cellulose binding domain, calmodulin binding peptide, an epitope tag, and combinations thereof, and wherein the affinity purification sequence remains attached to the protein of interest after cleaving said cleavage site.

15. (Previously presented) The method of claim 14, comprising affinity purifying the protein of interest after the separating step.

16. (Previously presented) A method for screening a plurality of potential binding partners for binding to a protein of interest, the method comprising:

(a) obtaining a cell transformed to express a fusion protein, said fusion protein comprising:

(i) said protein of interest; and

(ii) a single post-translational modification sequence;

(b) growing said cell or progeny of said cell under conditions which permit expression and post-translation modification of said fusion protein to produce a singly tagged fusion protein;

(c) introducing into the cell the plurality of potential binding partners;

(d) contacting an extract of said cell or progeny of said cell with an affinity purification reagent which specifically binds to said tagged fusion protein to form a complex;

(e) separating said complex from said extract; and

(f) identifying said potential binding partner as a binding partner if said potential binding partner binds said protein of interest in said complex.

17. (Original) The method of claim 16, wherein the plurality of potential binding partners are encoded by a plurality of nucleic acid expression vectors that when

introduced into the cell result in the expression in the cell of the plurality of potential binding partners.

18. (Withdrawn) An expression vector encoding a fusion protein, wherein the fusion protein comprises a protein of interest and a post-translational modification sequence.

19. (Withdrawn) A cell comprising the expression vector of claim 18.